

FIG. 1A-1
FIG. 1A-2

FIG. 1A

39 (UPPER: SEQ ID NO.: 1)
19 (LOWER: SEQ ID NO.: 4)

GAAATCCCCAACAGAGCCAAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC

119
39 1/20

TTCCCTTCACTACAAACTTCATTGCTTGGCCAAAAGAGAGTTAATTCATGTAGACAT

179
59

CTATGTAGGCAATTAAAAAACCCTATTGATGTATAAAACAGTTTCATTTCATCGGAGGGCAAC

239
79

TAAATACATTCTAGGACTTTATAAAAGATCACTTTTATTATTATGCACAGGGTGGAAACAAG

299
99

ATGGATTATCAAGTCTCAAGTCCAAATCTATGACATCAATTTATTATACATCGGAGCCCTGC
M D Y Q V S S P I Y D I N Y Y T S E P C

FIG. 1A-1

359	CAAAAATCAATGAAGCAATCGCGCCGCTCCTGCTCCGCTCTACTCACTGGTG
119	Q K I N V K Q I A A R L L P P L Y S L V
419	TTCACTTTGGTTTGGGCAACATGCTGGTCATCCTCATCTGATATAAAGTCAAAAGG
139	F I F G F V G N M L V I L I L I N C K R
479	CTGAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCCTT
159	L K S M T D I Y L L N L A I S D L F F L
539	CTTACTGTCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAATG
179	L T V P F W A H Y A A A Q W D F G N T M
599	TGTCACCTCTTGACAGGGCTCTATTTTATAGGCTTCTCTCTGGAATCTTCTTCTATCATC
199	C Q L L T G L Y F I G F F S G I F F I I
659	CTCCTGACATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCCTTAAAGCCAGG
219	L L T I D R Y L A V V H A V F A L K A R
719	ACGGTCACCTTTGGGGTGGTGAAGTGTGATCATTGGGTGGGCTGTGTTGGGTCT
239	T V T F G V V T S V I T W V V A V F A S
779	CTCCCGGAATCATCTTTACCAATCTCAAAAAGAGGTCTTCAATTACACCTGCAGCTCT
259	L P G I I F T R S Q K E G L H Y T C S S

CATTTTCATACA
H F P Y

FIG. 1A-2

FIG. 1B-1
FIG. 1B-2

FIG. 1B

GAAATCCCCCAACAGAGCCAGCTCTCCATCTAGTGACAGGGAAGCTAGCAGCAAAACC 59 (UPPER: SEQ ID NO.: 2)
19 (LOWER: SEQ ID NO.: 5)

TTCCCTTCACTACAAAACCTTCATTGCTTGCCCAAAAGAGAGCTTAATTCATGTAGACAT 119
39 3/20

CTATGTAGGCAATTAAAAACCTATTGATGTATATAAACAGATTGTCATTCATGGAGGGCAAC 179
59

TAAATACATTCTAGGACTTTATATAAAGATCATTTTTATTATGCACAGGGTGGACAAAG 239
79

ATGGATTATCAAGTCAAGTCCATCTATGACATCAATTTATATACATCGGAGCCCTGC 299
M D Y Q V S S P I Y D I N Y Y T S E P C 99

FIG. 1B-1

CAAAAAATCAATGTGAAGCAAAATCGCAGCCCGCTCCTCCCTCGCTCTACTCACTGGTG 359
 Q K I N V K Q I A A R L L P P L Y S L V 119
 TTCACTCTTTGGTTTGGGCAACATGCTGGTCACTCCTCATCTCATGATAAACTGCAAAAGG 419
 F I F G F V G N M L V I L I L I N C K R 139
 CTGAAGAGCATGACATCTACTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT 479
 L K S M T D I Y L L N L A I S D L F F L 159
 CTTACTGTCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAATACAATG 539
 L T V P F W A H Y A A A Q W D F G N T M 179
 TGTCAACTCTTGACAGGCTCTATTATTATAGGCTTCTCTGGAATCTTCTTCATCATC 599
 C Q L L T G L Y F I G F F S G I F F I I 199
 CTCCTGACAAATCGATAGGTACCTGGCTGCTGCCATGCTGTGTTTGTCTTAAAGCCAGG 659
 L L T I D R Y L A V V H A V F A L K A R 219
 ACGGTACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGGCTGTGTTTGGCTCT 719
 T V T F G V V T S V I T W V V A V F A S 239
 CTCACAGGAATCATCTTTACCATGATCTCAAAAGAAGGTCTTCAATTACACCTGCAGCTCT 779
 L P G I I F T R S Q K E G L H Y T C S S 259
 CATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTCCAGACATTAAGATAGTCAATC 839
 H F P Y S Q Y Q F W K N F Q T L K I V I 279

TTGGGGGTGCTCCTCGCGCTGCTTGTCTCATGTGTCATCTGCTACTCGGGAATCCTAAAACT 899
 L G L V L P L L V M V I C Y S G I L K T 299
 CTGCTTCGGTGTGGAATCAGAGAAGAGGCACAGGGCTGTAGGCTTATCTTCACCATC 959
 L L R C R N E K K R H R A V R L I F T I 319
 ATGATGTGTTATTTCTCTCTGGCTCCCTACAACATGTGCTCTCTCTGAACACCTTC 1019
 M I V Y F L F W A P Y N I V L L L N T F 339
 CAGGAATCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCAG 1079
 Q E F F G L N N C S S S N R L D Q A M Q 359
 GTGACAGAGACTCTTGGGATCAGCGACTGCTGCATCAACCCCATCATCTATGCTTTGTC 1139
 V T E T L G M T H C C I N P I I Y A F V 379
 GGGGAGAAGTTCAGAACTACTCTTAGTCTCTTCCAAAAGCACATTCGCCAACGTTTC 1199
 G E K F R N Y L L V F F Q K H I A K R F 399
 TGCAAAATGCTGTTCTATTTCCAGCAAGAGGCTCCGAGCGAGCAAGCTCAGTTTACACC 1259
 C K C C S I F Q Q E A P E R A S S V Y T 419
 CGATCCACTGGGAGCAGGAATAATCTGTGGGCTTGTCACGCACTCAAGTGGGCTGCT 1319
 R S T G E Q E I S V G L * 439
 GACCCAGTCAGAGTTGTGCATGGCTTAGTTTTCTATACACAGCCCTGGGCTGGGGTNGG 1379
 459
 TTGNNAGGCTCTTTTTTAAAGGAAGTTACTGTATTAGAGGGTCTAAGATTCATCCATT 1439
 479
 TATTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC

FIG. 1B-3

FIG. 1D-1
FIG. 1D-2

FIG. 1D

GAA TTC C C C C C A A C A G A G C C A G C T C C C A T C T A G T G G A C A G G A A G C T A G C A G C A A A C C
 59 (UPPER: SEQ ID NO. 3)
 19 (LOWER: SEQ ID NO. 6)

T T C C C T T C A C T A C A A A C T T C A T T G C T T G G C C A A A A G A G A G T T A A T T C A A T G T A C A C A T
 119
 39

C T A T G T A G G C A A T T A A A A C C T A T T G A T G T A T A A A C A G T T T G C A T T C A T G G A G G G C A A C
 179
 59

T A A A T A C A T T C T A G G A C T T T A T A A A A G A T C A C T T T T T A T T A T T A T G C A C A G G G T G A A C A A G
 239
 79

A T G G A T T A T C A A G T G T C A A G T C C A A T C T A T A G A C A T C A A T T A T T A T A C A T C G G A G C C C T G C
 299
 99
 M D Y Q V S S P I Y D I N Y Y T S E P C

FIG. 1D-1

359 CAAAAATCAATGTGAAGCAAAATCGAGCCGCTCCTGCTCCGCTCTACTCACTGTG
 119 Q K I N V K Q I A A R L L P P L Y S L V
 419 TTCACTCTTTGGTTTGTGGCAACATGCTGTCTATCTCTCACTCTGATTAATACTGCAAAAGG
 139 F I F G F V G N M L V I L I L I N C K R
 479 CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCCTT
 159 L K S M T D I Y L L N L A I S D L F L
 539 CTTACTCTCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGACCTTGGAAATACAATG
 179 L T V P F W A H Y A A A Q W D F G N T M
 599 TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTCTCTGGAATCTTCTTCATCATC
 199 C Q L L T G L Y F I G F F S G I F I I
 659 CTCCTGACAAATCGATAGGTACCTGGCTGTCTGCCATGCTGTGTTTGTCTTAAAGCCAGG
 219 L L T I D R Y L A V V H A V F A L K A R
 719 ACGGTCACTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGTGTGTTGGGTCT
 239 T V T F G V V T S V I T W V V A V F A S
 779 CTCGCCAGGAATCATCTTTTACCAGATCTCAAAAAGAGTCTTCAATTACACCTGCAGCTCT
 259 L P G I I F T R S Q K E G L H Y T C S S
 839 CATTTTCCATACATTAAAGATAGTCACTTGGGGTGGTCTCGCGGTGCTTGTATGTT
 279 H F P Y I K D S H L G A G P A A A C H G

FIG. 1D-2

CATCTGTACTCGGGAATCCTAAACACTCTGCTTCGGTGTGGAATGAGAAGAGAGGCA 899
 H L L G N P K N S A S V S K * 299
 CAGGGCTGTAGGCTTATCTTCACCATCATGATTGTTTATTCTCTCTCTGGGCTCCCTA 959
 319
 CAACATTGTCTTCTCTCTGAAACACTTCCAGGAATTCTTTGGCCCTGGAATAATTGCAGTAG 1019
 339
 CTTTAAAGGTTGGACCAAGCTATGCAGGTGCAGAGACTCTTTGGGATCAGCCACTGCTG 1079
 359
 CATCAACCCCATCATCTATGCCCTTTGTTCGGGAGAAAGTTCAGAAACTACCTCTTAGTCTTT 1139
 379
 CTTCCAAAGCACAATTGCCAAACGCTTCTGCAAAATGCTGTTCTATTTTCCAGCAAGAGGC 1199
 399
 TCCCGAGCGCAGCAAGCTCAGTTTACACCGATCCACTGGGGAGCAGGAATATCTCTGTGGG 1259
 419
 CTTGTGCACGGACTCAAGTGGGCTGTTGACCCAGTCAGAGTTCTGCACATGGCTTAGTT 1319
 439
 TTATATACAGCGCTGGGCTGGGGTNGGTTGGNNGAGGCTTTTTTTTAAAGGAAGTTACT 1379
 459
 GTTATAGAGGGTCTAAGATTCAATCCATTATTTGGCATCTGTTTAAAGTAGATTAGATCC 1439
 479

GAATTC

FIG. 1D-3

FIG. 2A
FIG. 2B

FIG. 2

	I	II
CCR5	1 MDYQVSSPTIDINVTSEPCQKINVKQIMARLLPPLYSLVFTFGVGNMLMILLINCKRLKSMTDIYLLNLAISDIFLLIT	83
hcc-R2b	6 MLSTSRSRFRINTNESGEVTTFFDYDGAPOHNEVVKQIGALLPPLYSLVFTFGVGNMLWLLINCKRLKCLTDIYLLNLAISDILFLLIT	95
hcc-R3	MTTSLDTVEFTFGTYYDDVGLLDEADTRALMAQFVPPPLYSLVFTVGLIGNVWWMILKKVRURIMTNIYLLNLAISDILFLLIT	87
hcc-R1	METPPNTTDDYDTTTEFDVGDATPCQKWNERRAFGALLPPLYSLVFVIGLVGNLWLVQVKKRLKNTSIYLLNLAISDILFLLIT	87
hcc-R4	MNPDTADTTLDESYSNMYLYESIPKPTKEGIRAFGEFLPPLYSLVFVFEGLGNSWVWVFKKRLRSMTDVILLNLAISDILFVFS	92
	III	IV
CCR5	VFFWAHYAARQMDFGNTMOQLLTGLYFIIGFTSGIFFIILLTIDRYIAVHAVFALKARTVTGCVTSVITWVAVFASLPGIIFTRQKEGIIH	177
hcc-R2b	LPLWAHSAANENWFGNACKLFTGLYHIGYFGGIFILLTIDRYIAVHAVFALKARTVTGCVTSVITWVAVFASLPGIIFTRQKEDSV	189
hcc-R3	LPLFWHVGHNWFGHGNLISEFHTGLYSEIFFIILLTIDRYIAVHAVFALKARTVTGCVTSVITWGLAVFALPELFTETEELFEE	182
hcc-R1	LPLFMDKLKDMWFGDAMOKILSEFNTGLYSEIFFIILLTIDRYIAVHAVFALKARTVTGCVTSITWGLALLASLPGLYFSKQMEFTFH	182
hcc-R4	LPLFWGNYAADQWFEGLGICKMISWMLVGFVSGIIFVLMKSIDRYIAVHAVFSLRARTVNGVHTSIATNSVAVFASLPGFTSTCTYENH	186

FIG. 2A

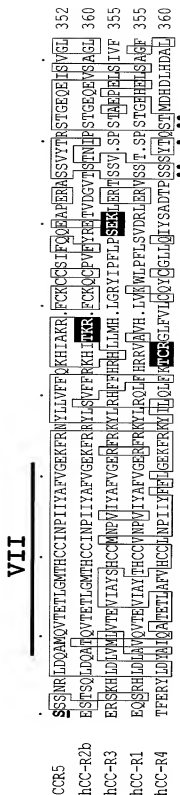
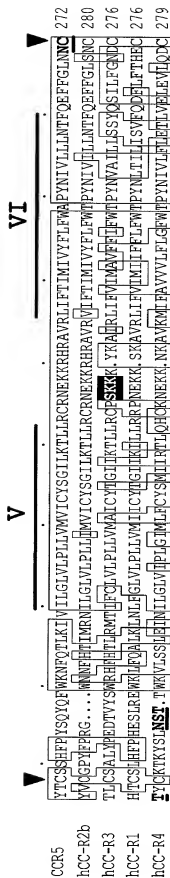


FIG. 2B

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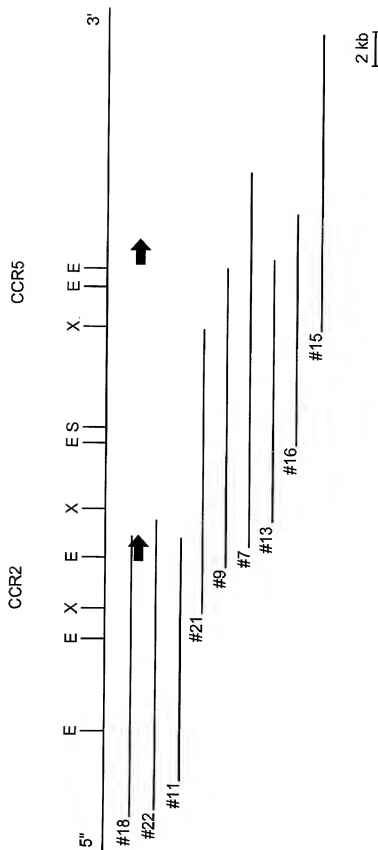


FIG. 3

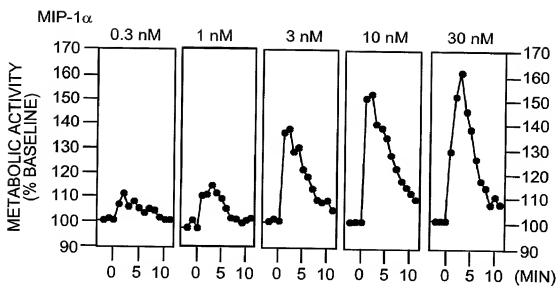


FIG. 4A

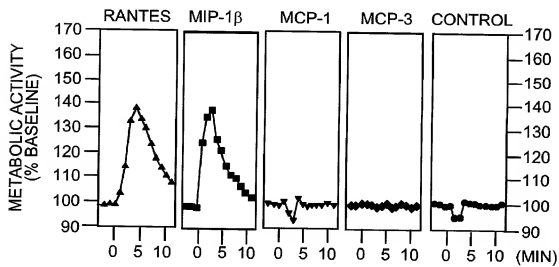


FIG. 4B

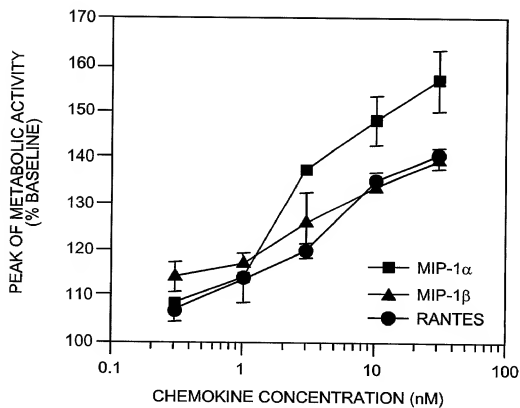


FIG. 4C



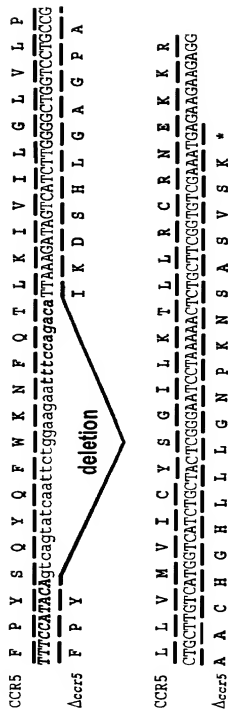


FIG. 6B

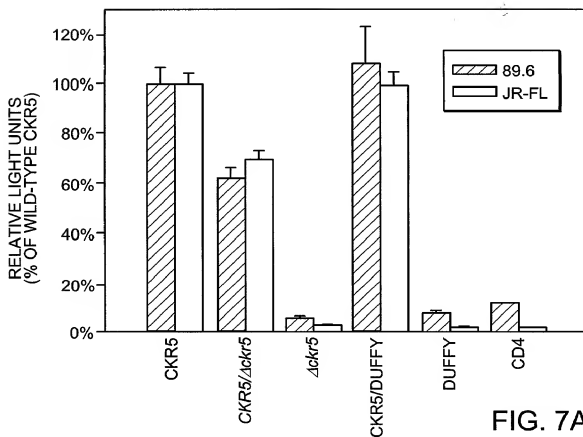


FIG. 7A

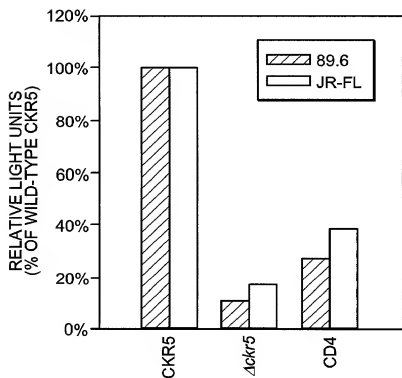


FIG. 7B

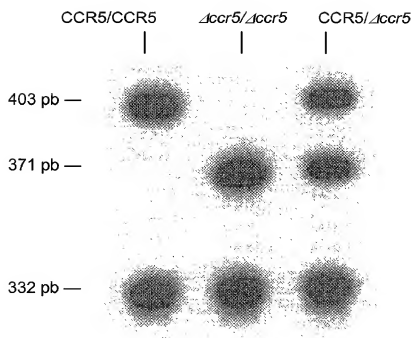


FIG. 8

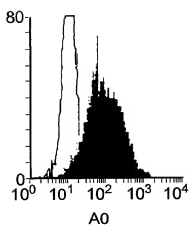


FIG. 9A

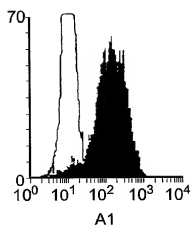


FIG. 9B

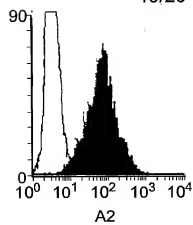


FIG. 9C

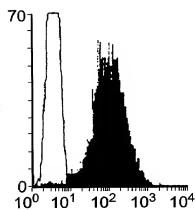


FIG. 9D

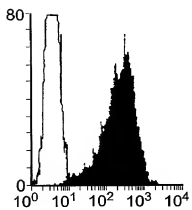


FIG. 9E

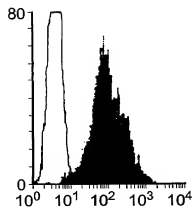


FIG. 9F

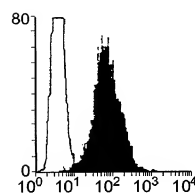


FIG. 9G

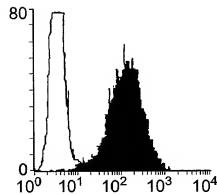


FIG. 9H

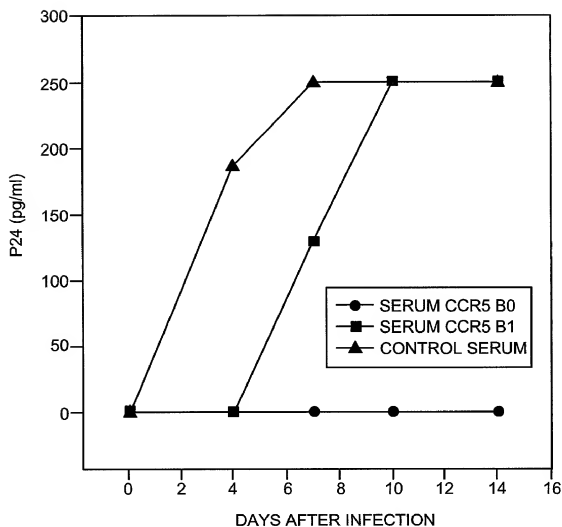


FIG. 10